

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: NAKAMURA, SEIJI
SAKURAI, TAKASHI
NEZU, JUNI-ICHI
- (ii) TITLE OF INVENTION: GENE ENCODING ADSEVERIN
- (iii) NUMBER OF SEQUENCES: 18
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Birch, Stewart, Kolasch & Birch, LLP
 - (B) STREET: P.O. Box 747
 - (C) CITY: Falls Church
 - (D) STATE: VA
 - (E) COUNTRY: USA
 - (F) ZIP: 22040-0747
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER:
 - (B) FILING DATE:
 - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: MURPHY Jr., Gerald M.
 - (B) REGISTRATION NUMBER: 28,977
 - (C) REFERENCE/DOCKET NUMBER: 230-110P
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: (703) 205-8000
 - (B) TELEFAX: (703) 205-8050

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 12 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Lys	Val	Ala	His	Val	Lys	Gln	Ile	Pro	Phe	Asp	Ala
1				5						10	

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 9 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Val Leu Thr Asn Asp Leu Thr Ala Gln
1 5

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 5 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Ile Thr Asn Arg Lys
1 5

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 2418 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 27..2171

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

CGGCCGGAAC ATCGCGTGCC CGAGTC ATG GCC CAG GGG CTG TAC CAC GAG GAG 53
 Met Ala Gln Gly Leu Tyr His Glu Glu
 1 5

TTC GCC CGC GCG GGC AAG CGG GCG GGG CTG CAG GTC TGG AGA ATT GAG 101

Phe	Ala	Arg	Ala	Gly	Lys	Arg	Ala	Gly	Leu	Gln	Val	Trp	Arg	Ile	Glu		
10					15					20					25		
AAG	CTG	GAG	CTG	GTG	CCG	GTG	CCC	GAG	AGC	GCG	TAT	GGC	AAC	TTC	TAC		149
Lys	Leu	Glu	Leu	Val	Pro	Val	Pro	Glu	Ser	Ala	Tyr	Gly	Asn	Phe	Tyr		
				30				35						40			
GTC	GGG	GAT	GCC	TAC	CTG	GTG	CTC	CAC	ACG	ACG	CAG	GCC	AGC	CGG	GGC		197
Val	Gly	Asp	Ala	Tyr	Leu	Val	Leu	His	Thr	Thr	Gln	Ala	Ser	Arg	Gly		
			45					50					55				
TTC	ACC	TAC	CGC	CTG	CAC	TTC	TGG	CTG	GGA	AAG	GAG	TGT	ACT	CAG	GAT		245
Phe	Thr	Tyr	Arg	Leu	His	Phe	Trp	Leu	Gly	Lys	Glu	Cys	Thr	Gln	Asp		
		60					65					70					
GAA	AGC	ACA	GCA	GCT	GCC	ATC	TTT	ACT	GTT	CAG	ATG	GAT	GAC	TAT	TTG		293
Glu	Ser	Thr	Ala	Ala	Ala	Ile	Phe	Thr	Val	Gln	Met	Asp	Asp	Tyr	Leu		
	75					80					85						
GGT	GGC	AAA	CCT	GTG	CAG	AAC	AGA	GAA	CTT	CAA	GGC	TAT	GAG	TCT	ACG		341
Gly	Gly	Lys	Pro	Val	Gln	Asn	Arg	Glu	Leu	Gln	Gly	Tyr	Glu	Ser	Thr		
	90				95					100					105		
GAT	TTT	GTT	GGC	TAC	TTT	AAA	GGA	GGT	CTG	AAA	TAC	AAG	GCT	GGC	GGT		389
Asp	Phe	Val	Gly	Tyr	Phe	Lys	Gly	Gly	Leu	Lys	Tyr	Lys	Ala	Gly	Gly		
				110					115					120			
GTG	GCG	TCT	GGA	CTC	AAT	CAT	GTG	CTT	ACA	AAT	GAC	TTG	ACT	GCT	CAG		437
Val	Ala	Ser	Gly	Leu	Asn	His	Val	Leu	Thr	Asn	Asp	Leu	Thr	Ala	Gln		
			125					130					135				
AGG	CTC	CTG	CAT	GTG	AAA	GGT	CGG	AGA	GTC	GTC	AGG	GCC	ACG	GAA	GTT		485
Arg.	Leu	Leu	His	Val	Lys	Gly	Arg	Arg	Val	Val	Arg	Ala	Thr	Glu	Val		
		140					145					150					
CCC	CTA	AGC	TGG	GAC	AGT	TTC	AAC	AAG	GGT	GAC	TGC	TTC	ATC	ATT	GAC		533
Pro	Leu	Ser	Trp	Asp	Ser	Phe	Asn	Lys	Gly	Asp	Cys	Phe	Ile	Ile	Asp		
	155					160					165						
CTT	GGC	ACT	GAA	ATT	TAC	CAG	TGG	TGT	GGA	TCT	TCT	TGC	AAC	AAG	TAC		581
Leu	Gly	Thr	Glu	Ile	Tyr	Gln	Trp	Cys	Gly	Ser	Ser	Cys	Asn	Lys	Tyr		
	170				175					180					185		
GAG	GCG	CTG	AAG	GCC	AGC	CAG	GTT	GCC	ATC	GGC	ATT	CGG	GAC	AAT	GAA		629
Glu	Arg	Leu	Lys	Ala	Ser	Gln	Val	Ala	Ile	Gly	Ile	Arg	Asp	Asn	Glu		
				190					195					200			
AGG	AAA	GGC	AGA	GCT	CAG	CTG	ATT	GTG	GTA	GAA	GAA	GGG	AGT	GAA	CCA		677
Arg	Lys	Gly	Arg	Ala	Gln	Leu	Ile	Val	Val	Glu	Glu	Gly	Ser	Glu	Pro		
			205					210					215				
TCA	GAG	CTT	ACA	AAG	GTA	TTA	GGG	GAA	AAG	CCA	AAG	CTT	AGG	GAT	GGA		725
Ser	Glu	Leu	Thr	Lys	Val	Leu	Gly	Glu	Lys	Pro	Lys	Leu	Arg	Asp	Gly		
		220					225					230					
GAA	GAT	GAT	GAT	GAC	ATC	AAA	GCA	GAT	ATA	ACT	AAT	AGG	AAA	ATG	GCT		773
Glu	Asp	Asp	Asp	Asp	Ile	Lys	Ala	Asp	Ile	Thr	Asn	Arg	Lys	Met	Ala		
	235					240					245						
AAA	CTC	TAC	ATG	GTT	TCA	GAT	GCC	AGT	GGC	TCC	ATG	AAA	GTG	AGT	CTG		821
Lys	Leu	Tyr	Met	Val	Ser	Asp	Ala	Ser	Gly	Ser	Met	Lys	Val	Ser	Leu		

250	255	260	265	
GTG GCA GAA GAA AAC CCC TTC TCC ATG GCG ATG CTT CTG TCT GAA GAA Val Ala Glu Glu Asn Pro Phe Ser Met Ala Met Leu Leu Ser Glu Glu 270 275 280				869
TGC TTC ATT TTG GAC CAC GGT GCT GCA AAA CAG ATT TTT GTA TGG AAA Cys Phe Ile Leu Asp His Gly Ala Ala Lys Gln Ile Phe Val Trp Lys 285 290 295				917
GGT AAA GAT GCT AAT CCC CAG GAG AGA AAG GCT GCC ATG AAG ACA GCT Gly Lys Asp Ala Asn Pro Gln Glu Arg Lys Ala Ala Met Lys Thr Ala 300 305 310				965
GAG GAA TTC CTA CAG CAA ATG AAT TAT TCT ACG AAT ACC CAA ATT CAA Glu Glu Phe Leu Gln Gln Met Asn Tyr Ser Thr Asn Thr Gln Ile Gln 315 320 325				1013
GTT CTT CCA GAA GGA GGT GAA ACA CCA ATC TTC AAA CAG TTC TTT AAG Val Leu Pro Glu Gly Gly Glu Thr Pro Ile Phe Lys Gln Phe Phe Lys 330 335 340 345				1061
GAC TGG AGA GAT AGA GAT CAG AGC GAT GGC TTC GGG AAA GTG TAT GTC Asp Trp Arg Asp Arg Asp Gln Ser Asp Gly Phe Gly Lys Val Tyr Val 350 355 360				1109
ACA GAA AAA GTG GCT CAC GTA AAA CAA ATT CCA TTT GAT GCC TCA AAA Thr Glu Lys Val Ala His Val Lys Gln Ile Pro Phe Asp Ala Ser Lys 365 370 375				1157
TTG CAC AGC TCC CCA CAA ATG GCA GCC CAG CAT CAC GTG GTG GAT GAC Leu His Ser Ser Pro Gln Met Ala Ala Gln His His Val Val Asp Asp 380 385 390				1205
GGT TCT GGC AAA GTG CAG ATT TGG CGT GTA GAA AAC AAC GGT AGG GTC Gly Ser Gly Lys Val Gln Ile Trp Arg Val Glu Asn Asn Gly Arg Val 395 400 405				1253
GAA ATT GAC CGA AAC TCG TAT GGT GAA TTC TAT GGT GGT GAT TGC TAC Glu Ile Asp Arg Asn Ser Tyr Gly Glu Phe Tyr Gly Gly Asp Cys Tyr 410 415 420 425				1301
ATT ATA CTT TAC ACT TAT CCC AGA GGA CAG ATT ATC TAC ACC TGG CAA Ile Ile Leu Tyr Thr Tyr Pro Arg Gly Gln Ile Ile Tyr Thr Trp Gln 430 435 440				1349
GGA GCA AAT GCC ACA CGG GAT GAG CTG ACA ACC TCC GCA TTC CTG ACT Gly Ala Asn Ala Thr Arg Asp Glu Leu Thr Thr Ser Ala Phe Leu Thr 445 450 455				1397
GTT CAG TTG GAT AGA TCC CTC GGG GGA CAG GCT GTG CAG ATT CGA GTC Val Gln Leu Asp Arg Ser Leu Gly Gly Gln Ala Val Gln Ile Arg Val 460 465 470				1445
TCC CAA GGC AAA GAA CCT GCT CAC CTG CTG AGT TTG TTC AAA GAC AAA Ser Gln Gly Lys Glu Pro Ala His Leu Leu Ser Leu Phe Lys Asp Lys 475 480 485				1493
CCG CTC ATT ATT TAC AAG AAC GGA ACA TCA AAG AAA GAA GGT CAG GCA Pro Leu Ile Ile Tyr Lys Asn Gly Thr Ser Lys Lys Glu Gly Gln Ala 490 495 500 505				1541

CCA GCC CCC CCT ATA CGC CTC TTT CAA GTC CGA AGA AAC CTG GCT TCG Pro Ala Pro Pro Ile Arg Leu Phe Gln Val Arg Arg Asn Leu Ala Ser 510 515 520	1589
ATC ACC AGA ATT ATG GAG GTA GAT GTT GAT GCA AAC TCA TTG AAT TCC Ile Thr Arg Ile Met Glu Val Asp Val Asp Ala Asn Ser Leu Asn Ser 525 530 535	1637
AAT GAT GTT TTT GTC CTG AAA CTG CGA CAA AAT AAT GGC TAC ATC TGG Asn Asp Val Phe Val Leu Lys Leu Arg Gln Asn Asn Gly Tyr Ile Trp 540 545 550	1685
ATA GGA AAA GGC TCC ACA CAG GAG GAG GAG AAA GGA GCA GAG TAC GTG Ile Gly Lys Gly Ser Thr Gln Glu Glu Glu Lys Gly Ala Glu Tyr Val 555 560 565	1733
GCA AGC GTC CTC AAA TGC AAA ACT TCG ACG ATT CAG GAA GGC AAG GAA Ala Ser Val Leu Lys Cys Lys Thr Ser Thr Ile Gln Glu Gly Lys Glu 570 575 580 585	1781
CCA GAG GAG TTT TGG AAT TCC CTT GGA GGG AAA AAA GAC TAC CAG ACC Pro Glu Glu Phe Trp Asn Ser Leu Gly Gly Lys Lys Asp Tyr Gln Thr 590 595 600	1829
TCT CCT CTG CTA GAA TCC CAG GCT GAA GAC CAT CCA CCT CGG CTT TAC Ser Pro Leu Leu Glu Ser Gln Ala Glu Asp His Pro Pro Arg Leu Tyr 605 610 615	1877
GGC TGC TCC AAC AAA ACT GGA AGA TTC ATT ATT GAA GAG GTT CCA GGA Gly Cys Ser Asn Lys Thr Gly Arg Phe Ile Ile Glu Glu Val Pro Gly 620 625 630	1925
GAG TTC ACC CAG GAT GAT TTA GCA GAA GAT GAT GTC ATG CTG TTA GAT Glu Phe Thr Gln Asp Asp Leu Ala Glu Asp Asp Val Met Leu Leu Asp 635 640 645	1973
GCT TGG GAA CAG ATT TTT ATT TGG ATT GGA AAA GAT GCC AAT GAA GTT Ala Trp Glu Gln Ile Phe Ile Trp Ile Gly Lys Asp Ala Asn Glu Val 650 655 660 665	2021
GAG AAA TCA GAA TCT CTG AAG TCT GCC AAA ATA TAC CTT GAG ACC GAC Glu Lys Ser Glu Ser Leu Lys Ser Ala Lys Ile Tyr Leu Glu Thr Asp 670 675 680	2069
CCT TCT GGA AGA GAC AAG AGG ACG CCA ATT GTC ATC ATA AAA CAG GGT Pro Ser Gly Arg Asp Lys Arg Thr Pro Ile Val Ile Ile Lys Gln Gly 685 690 695	2117
CAT GAG CCA CCT ACT TTC ACA GGC TGG TTC CTG GGC TGG GAT TCC AGC His Glu Pro Pro Thr Phe Thr Gly Trp Phe Leu Gly Trp Asp Ser Ser 700 705 710	2165
AGG TGG TAAACTGATT TTTGTAGGAA AAAACAAAT ATAATGGGGC AGCTGTCCCA Arg Trp 715	2221
GGGGGAAGG AGGAGCTTGT TTAACCTTAG AAAATTAACC TCAGCCATAT GGCTATTTTT	2281
CCGTGCTTAG AATTGGTTTG AAATTTCTTT TAACTGGAA TTTTCTTATG TTAATATTTT	2341

TATAACTTTT CTTATGGACC AATATTAGCT CTGCTGGATG CTGACATATC TTTATATATG 2401
 ACTTTTTTAAA GGGGCCG 2418

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 715 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Met	Ala	Gln	Gly	Leu	Tyr	His	Glu	Glu	Phe	Ala	Arg	Ala	Gly	Lys	Arg	1	5	10	15
Ala	Gly	Leu	Gln	Val	Trp	Arg	Ile	Glu	Lys	Leu	Glu	Leu	Val	Pro	Val	20	25	30	
Pro	Glu	Ser	Ala	Tyr	Gly	Asn	Phe	Tyr	Val	Gly	Asp	Ala	Tyr	Leu	Val	35	40	45	
Leu	His	Thr	Thr	Gln	Ala	Ser	Arg	Gly	Phe	Thr	Tyr	Arg	Leu	His	Phe	50	55	60	
Trp	Leu	Gly	Lys	Glu	Cys	Thr	Gln	Asp	Glu	Ser	Thr	Ala	Ala	Ala	Ile	65	70	75	80
Phe	Thr	Val	Gln	Met	Asp	Asp	Tyr	Leu	Gly	Gly	Lys	Pro	Val	Gln	Asn	85	90	95	
Arg	Glu	Leu	Gln	Gly	Tyr	Glu	Ser	Thr	Asp	Phe	Val	Gly	Tyr	Phe	Lys	100	105	110	
Gly	Gly	Leu	Lys	Tyr	Lys	Ala	Gly	Gly	Val	Ala	Ser	Gly	Leu	Asn	His	115	120	125	
Val	Leu	Thr	Asn	Asp	Leu	Thr	Ala	Gln	Arg	Leu	Leu	His	Val	Lys	Gly	130	135	140	
Arg	Arg	Val	Val	Arg	Ala	Thr	Glu	Val	Pro	Leu	Ser	Trp	Asp	Ser	Phe	145	150	155	160
Asn	Lys	Gly	Asp	Cys	Phe	Ile	Ile	Asp	Leu	Gly	Thr	Glu	Ile	Tyr	Gln	165	170	175	
Trp	Cys	Gly	Ser	Ser	Cys	Asn	Lys	Tyr	Glu	Arg	Leu	Lys	Ala	Ser	Gln	180	185	190	
Val	Ala	Ile	Gly	Ile	Arg	Asp	Asn	Glu	Arg	Lys	Gly	Arg	Ala	Gln	Leu	195	200	205	
Ile	Val	Val	Glu	Glu	Gly	Ser	Glu	Pro	Ser	Glu	Leu	Thr	Lys	Val	Leu	210	215	220	
Gly	Glu	Lys	Pro	Lys	Leu	Arg	Asp	Gly	Glu	Asp	Asp	Asp	Asp	Ile	Lys	225	230	235	240

Ala Asp Ile Thr Asn Arg Lys Met Ala Lys Leu Tyr Met Val Ser Asp
 245 250 255
 Ala Ser Gly Ser Met Lys Val Ser Leu Val Ala Glu Glu Asn Pro Phe
 260 265 270
 Ser Met Ala Met Leu Leu Ser Glu Glu Cys Phe Ile Leu Asp His Gly
 275 280 285
 Ala Ala Lys Gln Ile Phe Val Trp Lys Gly Lys Asp Ala Asn Pro Gln
 290 295 300
 Glu Arg Lys Ala Ala Met Lys Thr Ala Glu Glu Phe Leu Gln Gln Met
 305 310 315 320
 Asn Tyr Ser Thr Asn Thr Gln Ile Gln Val Leu Pro Glu Gly Gly Glu
 325 330 335
 Thr Pro Ile Phe Lys Gln Phe Phe Lys Asp Trp Arg Asp Arg Asp Gln
 340 345 350
 Ser Asp Gly Phe Gly Lys Val Tyr Val Thr Glu Lys Val Ala His Val
 355 360 365
 Lys Gln Ile Pro Phe Asp Ala Ser Lys Leu His Ser Ser Pro Gln Met
 370 375 380
 Ala Ala Gln His His Val Val Asp Asp Gly Ser Gly Lys Val Gln Ile
 385 390 395 400
 Trp Arg Val Glu Asn Asn Gly Arg Val Glu Ile Asp Arg Asn Ser Tyr
 405 410 415
 Gly Glu Phe Tyr Gly Gly Asp Cys Tyr Ile Ile Leu Tyr Thr Tyr Pro
 420 425 430
 Arg Gly Gln Ile Ile Tyr Thr Trp Gln Gly Ala Asn Ala Thr Arg Asp
 435 440 445
 Glu Leu Thr Thr Ser Ala Phe Leu Thr Val Gln Leu Asp Arg Ser Leu
 450 455 460
 Gly Gly Gln Ala Val Gln Ile Arg Val Ser Gln Gly Lys Glu Pro Ala
 465 470 475 480
 His Leu Leu Ser Leu Phe Lys Asp Lys Pro Leu Ile Ile Tyr Lys Asn
 485 490 495
 Gly Thr Ser Lys Lys Glu Gly Gln Ala Pro Ala Pro Pro Ile Arg Leu
 500 505 510
 Phe Gln Val Arg Arg Asn Leu Ala Ser Ile Thr Arg Ile Met Glu Val
 515 520 525
 Asp Val Asp Ala Asn Ser Leu Asn Ser Asn Asp Val Phe Val Leu Lys
 530 535 540
 Leu Arg Gln Asn Asn Gly Tyr Ile Trp Ile Gly Lys Gly Ser Thr Gln
 545 550 555 560
 Glu Glu Glu Lys Gly Ala Glu Tyr Val Ala Ser Val Leu Lys Cys Lys

	565		570		575
Thr Ser Thr	Ile Gln Glu Gly Lys	Glu Pro Glu Glu Phe Trp Asn Ser			
	580	585		590	
Leu Gly Gly	Lys Lys Asp Tyr Gln Thr Ser Pro Leu Leu Glu Ser Gln				
	595	600		605	
Ala Glu Asp	His Pro Pro Arg Leu Tyr Gly Cys Ser Asn Lys Thr Gly				
	610	615		620	
Arg Phe Ile Ile	Glu Glu Val Pro Gly Glu Phe Thr Gln Asp Asp Leu				
	625	630		635	640
Ala Glu Asp Asp	Val Met Leu Leu Asp Ala Trp Glu Gln Ile Phe Ile				
	645	650		655	
Trp Ile Gly	Lys Asp Ala Asn Glu Val Glu Lys Ser Glu Ser Leu Lys				
	660	665		670	
Ser Ala Lys Ile Tyr Leu Glu Thr Asp Pro Ser Gly Arg Asp Lys Arg					
	675	680		685	
Thr Pro Ile Val Ile Ile Lys Gln Gly His Glu Pro Pro Thr Phe Thr					
	690	695		700	
Gly Trp Phe Leu Gly Trp Asp Ser Ser Arg Trp					
	705	710		715	

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2630 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 79..2223

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

AAGGTTTCCTC CTGCTGCTCT CGGTTTAGTC CAAGATCAGC GATATCACGC GTCCCCCGGA	60
GCATCGCGTG CAGGAGCC ATG GCG CGG GAG CTA TAC CAC GAA GAG TTC GCC	111
Met Ala Arg Glu Leu Tyr His Glu Glu Phe Ala	
1 5 10	
CGG GCG GGC AAG CAG GCG GGG CTG CAG GTC TGG AGG ATT GAG AAG CTG	159
Arg Ala Gly Lys Gln Ala Gly Leu Gln Val Trp Arg Ile Glu Lys Leu	
15 20 25	
GAG CTG GTG CCC GTG CCC CAG AGC GCT CAC GGC GAC TTC TAC GTC GGG	207
Glu Leu Val Pro Val Pro Gln Ser Ala His Gly Asp Phe Tyr Val Gly	
30 35 40	

GAT	GCC	TAC	CTG	GTG	CTG	CAC	ACG	GCC	AAG	ACG	AGC	CGA	GGC	TTC	ACC	255
Asp	Ala	Tyr	Leu	Val	Leu	His	Thr	Ala	Lys	Thr	Ser	Arg	Gly	Phe	Thr	
45						50					55					
TAC	CAC	CTG	CAC	TTC	TGG	CTC	GGA	AAG	GAG	TGT	TCC	CAG	GAT	GAA	AGC	303
Tyr	His	Leu	His	Phe	Trp	Leu	Gly	Lys	Glu	Cys	Ser	Gln	Asp	Glu	Ser	
60					65				70					75		
ACA	GCT	GCT	GCC	ATC	TTC	ACT	GTT	CAG	ATG	GAT	GAC	TAT	TTG	GGT	GGC	351
Thr	Ala	Ala	Ala	Ile	Phe	Thr	Val	Gln	Met	Asp	Asp	Tyr	Leu	Gly	Gly	
				80					85					90		
AAG	CCA	GTG	CAG	AAT	AGA	GAA	CTT	CAA	GGA	TAT	GAG	TCT	AAT	GAC	TTT	399
Lys	Pro	Val	Gln	Asn	Arg	Glu	Leu	Gln	Gly	Tyr	Glu	Ser	Asn	Asp	Phe	
			95					100					105			
GTT	AGC	TAT	TTC	AAA	GGC	GGT	CTG	AAA	TAC	AAG	GCT	GGA	GGC	GTG	GCA	447
Val	Ser	Tyr	Phe	Lys	Gly	Gly	Leu	Lys	Tyr	Lys	Ala	Gly	Gly	Val	Ala	
		110					115					120				
TCT	GGA	TTA	AAT	CAT	GTT	CTT	ACG	AAC	GAC	CTG	ACA	GCC	AAG	AGG	CTC	495
Ser	Gly	Leu	Asn	His	Val	Leu	Thr	Asn	Asp	Leu	Thr	Ala	Lys	Arg	Leu	
	125					130					135					
CTA	CAT	GTG	AAG	GGT	CGT	AGA	GTG	GTG	AGA	GCC	ACA	GAA	GTT	CCC	CTT	543
Leu	His	Val	Lys	Gly	Arg	Arg	Val	Val	Arg	Ala	Thr	Glu	Val	Pro	Leu	
140					145					150					155	
AGC	TGG	GAC	AGT	TTC	AAC	AAG	GGT	GAC	TGC	TTC	ATC	ATT	GAC	CTT	GGC	591
Ser	Trp	Asp	Ser	Phe	Asn	Lys	Gly	Asp	Cys	Phe	Ile	Ile	Asp	Leu	Gly	
				160					165					170		
ACC	GAA	ATT	TAT	CAG	TGG	TGT	GGT	TCC	TCG	TGC	AAC	AAA	TAT	GAA	CGT	639
Thr	Glu	Ile	Tyr	Gln	Trp	Cys	Gly	Ser	Ser	Cys	Asn	Lys	Tyr	Glu	Arg	
			175					180					185			
CTG	AAG	GCA	AAC	CAG	GTA	GCT	ACT	GGC	ATT	CGG	TAC	AAT	GAA	AGG	AAA	687
Leu	Lys	Ala	Asn	Gln	Val	Ala	Thr	Gly	Ile	Arg	Tyr	Asn	Glu	Arg	Lys	
		190					195					200				
GGA	AGG	TCT	GAA	CTA	ATT	GTC	GTG	GAA	GAA	GGA	AGT	GAA	CCC	TCA	GAA	735
Gly	Arg	Ser	Glu	Leu	Ile	Val	Val	Glu	Glu	Gly	Ser	Glu	Pro	Ser	Glu	
	205					210					215					
CTT	ATA	AAG	GTC	TTA	GGG	GAA	AAG	CCA	GAG	CTT	CCA	GAT	GGA	GGT	GAT	783
Leu	Ile	Lys	Val	Leu	Gly	Glu	Lys	Pro	Glu	Leu	Pro	Asp	Gly	Gly	Asp	
220					225					230					235	
GAT	GAT	GAC	ATT	ATA	GCA	GAC	ATA	AGT	AAC	AGG	AAA	ATG	GCT	AAA	CTA	831
Asp	Asp	Asp	Ile	Ile	Ala	Asp	Ile	Ser	Asn	Arg	Lys	Met	Ala	Lys	Leu	
				240					245					250		
TAC	ATG	GTT	TCA	GAT	GCA	AGT	GGC	TCC	ATG	AGA	GTG	ACT	GTG	GTG	GCA	879
Tyr	Met	Val	Ser	Asp	Ala	Ser	Gly	Ser	Met	Arg	Val	Thr	Val	Val	Ala	
			255					260					265			
GAA	GAA	AAC	CCC	TTC	TCA	ATG	GCA	ATG	CTG	CTG	TCT	GAA	GAA	TGC	TTT	927
Glu	Glu	Asn	Pro	Phe	Ser	Met	Ala	Met	Leu	Leu	Ser	Glu	Glu	Cys	Phe	
		270					275					280				

ATT TTG GAC CAC GGG GCT GCC AAA CAA ATT TTC GTA TGG AAA GGT AAA Ile Leu Asp His Gly Ala Ala Lys Gln Ile Phe Val Trp Lys Gly Lys 285 290 295	975
GAT GCT AAT CCC CAA GAG AGG AAG GCT GCA ATG AAG ACA GCT GAA GAA Asp Ala Asn Pro Gln Glu Arg Lys Ala Ala Met Lys Thr Ala Glu Glu 300 305 310 315	1023
TTT CTA CAG CAA ATG AAT TAT TCC AAG AAT ACC CAA ATT CAA GTT CTT Phe Leu Gln Gln Met Asn Tyr Ser Lys Asn Thr Gln Ile Gln Val Leu 320 325 330	1071
CCA GAA GGA GGT GAA ACA CCA ATC TTC AAA CAG TTT TTT AAG GAC TGG Pro Glu Gly Gly Glu Thr Pro Ile Phe Lys Gln Phe Phe Lys Asp Trp 335 340 345	1119
AGA GAT AAA GAT CAG AGT GAT GGC TTC GGG AAA GTT TAT GTC ACA GAG Arg Asp Lys Asp Gln Ser Asp Gly Phe Gly Lys Val Tyr Val Thr Glu 350 355 360	1167
AAA GTG GCT CAA ATA AAA CAA ATT CCC TTT GAT GCC TCA AAA TTA CAC Lys Val Ala Gln Ile Lys Gln Ile Pro Phe Asp Ala Ser Lys Leu His 365 370 375	1215
AGT TCT CCG CAG ATG GCA GCC CAG CAC AAT ATG GTG GAT GAT GGT TCT Ser Ser Pro Gln Met Ala Ala Gln His Asn Met Val Asp Asp Gly Ser 380 385 390 395	1263
GGC AAA GTG GAG ATT TGG CGT GTA GAA AAC AAT GGT AGG ATC CAA GTT Gly Lys Val Glu Ile Trp Arg Val Glu Asn Asn Gly Arg Ile Gln Val 400 405 410	1311
GAC CAA AAC TCA TAT GGT GAA TTC TAT GGT GGT GAC TGC TAC ATC ATA Asp Gln Asn Ser Tyr Gly Glu Phe Tyr Gly Gly Asp Cys Tyr Ile Ile 415 420 425	1359
CTC TAC ACC TAT CCC AGA GGA CAG ATT ATC TAC ACG TGG CAA GGA GCA Leu Tyr Thr Tyr Pro Arg Gly Gln Ile Ile Tyr Thr Trp Gln Gly Ala 430 435 440	1407
AAT GCC ACA CGA GAT GAG CTG ACA ACA TCT GCG TTC CTG ACT GTT CAG Asn Ala Thr Arg Asp Glu Leu Thr Thr Ser Ala Phe Leu Thr Val Gln 445 450 455	1455
TTG GAT CGG TCC CTT GGA GGA CAG GCT GTG CAG ATC CGA GTC TCC CAA Leu Asp Arg Ser Leu Gly Gly Gln Ala Val Gln Ile Arg Val Ser Gln 460 465 470 475	1503
GGC AAA GAG CCT GTT CAC CTA CTG AGT TTG TTC AAA GAC AAA CCG CTC Gly Lys Glu Pro Val His Leu Leu Ser Leu Phe Lys Asp Lys Pro Leu 480 485 490	1551
ATT ATT TAC AAG AAT GGA ACA TCA AAG AAA GGA GGT CAG GCA CCT GCT Ile Ile Tyr Lys Asn Gly Thr Ser Lys Lys Gly Gly Gln Ala Pro Ala 495 500 505	1599
CCC CCT ACA CGC CTC TTT CAA GTC CGG AGA AAC CTG GCA TCT ATC ACC Pro Pro Thr Arg Leu Phe Gln Val Arg Arg Asn Leu Ala Ser Ile Thr 510 515 520	1647
AGA ATT GTG GAG GTT GAT GTT GAT GCA AAT TCA CTG AAT TCT AAC GAT	1695

Arg	Ile	Val	Glu	Val	Asp	Val	Asp	Ala	Asn	Ser	Leu	Asn	Ser	Asn	Asp		
525						530					535						
GTT	TGT	GTC	CTG	AAA	CTG	CCA	CAA	AAT	AGT	GGC	TAC	ATC	TGG	GTA	GGA	1743	
Val	Cys	Val	Leu	Lys	Leu	Pro	Gln	Asn	Ser	Gly	Tyr	Ile	Trp	Val	Gly		
540					545					550					555		
AAA	GGT	GCT	AGC	CAG	GAG	GAG	GAG	AAA	GGA	GCA	GAG	TAT	GTA	GCA	AGT	1791	
Lys	Gly	Ala	Ser	Gln	Glu	Glu	Glu	Lys	Gly	Ala	Glu	Tyr	Val	Ala	Ser		
				560					565						570		
GTC	CTA	AAG	TGC	AAA	ACC	TTA	AGG	ATC	CAA	GAA	GGC	GAG	GAG	CCA	GAG	1839	
Val	Leu	Lys	Cys	Lys	Thr	Leu	Arg	Ile	Gln	Glu	Gly	Glu	Glu	Pro	Glu		
			575					580						585			
GAG	TTC	TGG	AAT	TCC	CTT	GGA	GGG	AAA	AAA	GAC	TAC	CAG	ACC	TCA	CCA	1887	
Glu	Phe	Trp	Asn	Ser	Leu	Gly	Gly	Lys	Lys	Asp	Tyr	Gln	Thr	Ser	Pro		
			590				595					600					
CTA	CTG	GAA	ACC	CAG	GCT	GAA	GAC	CAT	CCA	CCT	CGG	CTT	TAC	GGC	TGC	1935	
Leu	Leu	Glu	Thr	Gln	Ala	Glu	Asp	His	Pro	Pro	Arg	Leu	Tyr	Gly	Cys		
	605					610					615						
TCT	AAC	AAA	ACT	GGA	AGA	TTT	GTT	ATT	GAA	GAG	ATT	CCA	GGA	GAG	TTC	1983	
Ser	Asn	Lys	Thr	Gly	Arg	Phe	Val	Ile	Glu	Glu	Ile	Pro	Gly	Glu	Phe		
620					625					630					635		
ACC	CAG	GAT	GAT	TTA	GCT	GAA	GAT	GAT	GTC	ATG	TTA	CTA	GAT	GCT	TGG	2031	
Thr	Gln	Asp	Asp	Leu	Ala	Glu	Asp	Asp	Val	Met	Leu	Leu	Asp	Ala	Trp		
				640					645					650			
GAA	CAG	ATA	TTT	ATT	TGG	ATT	GGC	AAA	GAT	GCT	AAT	GAA	GTT	GAG	AAA	2079	
Glu	Gln	Ile	Phe	Ile	Trp	Ile	Gly	Lys	Asp	Ala	Asn	Glu	Val	Glu	Lys		
			655					660					665				
AAA	GAA	TCT	CTG	AAG	TCT	GCC	AAA	ATG	TAC	CTT	GAG	ACA	GAC	CCT	TCT	2127	
Lys	Glu	Ser	Leu	Lys	Ser	Ala	Lys	Met	Tyr	Leu	Glu	Thr	Asp	Pro	Ser		
		670					675					680					
GGA	AGA	GAC	AAG	AGG	ACA	CCA	ATT	GTC	ATC	ATA	AAA	CAG	GGC	CAT	GAG	2175	
Gly	Arg	Asp	Lys	Arg	Thr	Pro	Ile	Val	Ile	Ile	Lys	Gln	Gly	His	Glu		
		685				690					695						
CCA	CCC	ACA	TTC	ACA	GGC	TGG	TTC	CTG	GGC	TGG	GAT	TCC	AGC	AAG	TGG	2223	
Pro	Pro	Thr	Phe	Thr	Gly	Trp	Phe	Leu	Gly	Trp	Asp	Ser	Ser	Lys	Trp		
700					705					710					715		
TAAATTGGTA	TTTGTAAAAA	GCAAACAAAC	ATTACAAGGC	AGTTATCTCA	TTGCTGTTTT	2283											
GGGAGAGGAA	CGGGAAAAGC	TTTTTGCTTA	TTTGTCTTTT	GAAAATTAAG	GCTGGGCGCG	2343											
GTGGCTCACA	CCTGTAATCC	CAGCACTTTG	AGAGGATGAG	GTAGGCGGAT	CACTGGGGTC	2403											
AGGATTTCGA	GACCAGCCTG	GCCAACATGG	CGAAACCTCG	CCTCTACTAA	AAATACAAAA	2463											
AAATTAGCTG	CGCGTGGTGG	TGCACGCCTG	TAGTCCCTGC	TACTTGGAAG	GCTGAGACAG	2523											
GAAAATTGCT	TGAGCCCAGG	AGGCTGAGGT	TGCAGTGAGC	CAGGATTGCG	CCACCACACT	2583											
CCAGCCTGGG	CAACAGAGAC	TCTGTCTCAA	AAAAAAAAAA	AAAAAAA		2630											

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 715 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Met Ala Arg Glu Leu Tyr His Glu Glu Phe Ala Arg Ala Gly Lys Gln
1 5 10 15
Ala Gly Leu Gln Val Trp Arg Ile Glu Lys Leu Glu Leu Val Pro Val
20 25 30
Pro Gln Ser Ala His Gly Asp Phe Tyr Val Gly Asp Ala Tyr Leu Val
35 40 45
Leu His Thr Ala Lys Thr Ser Arg Gly Phe Thr Tyr His Leu His Phe
50 55 60
Trp Leu Gly Lys Glu Cys Ser Gln Asp Glu Ser Thr Ala Ala Ala Ile
65 70 75 80
Phe Thr Val Gln Met Asp Asp Tyr Leu Gly Gly Lys Pro Val Gln Asn
85 90 95
Arg Glu Leu Gln Gly Tyr Glu Ser Asn Asp Phe Val Ser Tyr Phe Lys
100 105 110
Gly Gly Leu Lys Tyr Lys Ala Gly Gly Val Ala Ser Gly Leu Asn His
115 120 125
Val Leu Thr Asn Asp Leu Thr Ala Lys Arg Leu Leu His Val Lys Gly
130 135 140
Arg Arg Val Val Arg Ala Thr Glu Val Pro Leu Ser Trp Asp Ser Phe
145 150 155 160
Asn Lys Gly Asp Cys Phe Ile Ile Asp Leu Gly Thr Glu Ile Tyr Gln
165 170 175
Trp Cys Gly Ser Ser Cys Asn Lys Tyr Glu Arg Leu Lys Ala Asn Gln
180 185 190
Val Ala Thr Gly Ile Arg Tyr Asn Glu Arg Lys Gly Arg Ser Glu Leu
195 200 205
Ile Val Val Glu Glu Gly Ser Glu Pro Ser Glu Leu Ile Lys Val Leu
210 215 220
Gly Glu Lys Pro Glu Leu Pro Asp Gly Gly Asp Asp Asp Asp Ile Ile
225 230 235 240
Ala Asp Ile Ser Asn Arg Lys Met Ala Lys Leu Tyr Met Val Ser Asp
245 250 255
Ala Ser Gly Ser Met Arg Val Thr Val Val Ala Glu Glu Asn Pro Phe

260					265					270					
Ser	Met	Ala	Met	Leu	Leu	Ser	Glu	Glu	Cys	Phe	Ile	Leu	Asp	His	Gly
		275					280					285			
Ala	Ala	Lys	Gln	Ile	Phe	Val	Trp	Lys	Gly	Lys	Asp	Ala	Asn	Pro	Gln
		290					295					300			
Glu	Arg	Lys	Ala	Ala	Met	Lys	Thr	Ala	Glu	Glu	Phe	Leu	Gln	Gln	Met
305							310					315			320
Asn	Tyr	Ser	Lys	Asn	Thr	Gln	Ile	Gln	Val	Leu	Pro	Glu	Gly	Gly	Glu
				325					330					335	
Thr	Pro	Ile	Phe	Lys	Gln	Phe	Phe	Lys	Asp	Trp	Arg	Asp	Lys	Asp	Gln
			340						345					350	
Ser	Asp	Gly	Phe	Gly	Lys	Val	Tyr	Val	Thr	Glu	Lys	Val	Ala	Gln	Ile
		355					360					365			
Lys	Gln	Ile	Pro	Phe	Asp	Ala	Ser	Lys	Leu	His	Ser	Ser	Pro	Gln	Met
		370					375					380			
Ala	Ala	Gln	His	Asn	Met	Val	Asp	Asp	Gly	Ser	Gly	Lys	Val	Glu	Ile
385							390					395			400
Trp	Arg	Val	Glu	Asn	Asn	Gly	Arg	Ile	Gln	Val	Asp	Gln	Asn	Ser	Tyr
				405					410					415	
Gly	Glu	Phe	Tyr	Gly	Gly	Asp	Cys	Tyr	Ile	Ile	Leu	Tyr	Thr	Tyr	Pro
			420						425					430	
Arg	Gly	Gln	Ile	Ile	Tyr	Thr	Trp	Gln	Gly	Ala	Asn	Ala	Thr	Arg	Asp
			435						440					445	
Glu	Leu	Thr	Thr	Ser	Ala	Phe	Leu	Thr	Val	Gln	Leu	Asp	Arg	Ser	Leu
			450				455					460			
Gly	Gly	Gln	Ala	Val	Gln	Ile	Arg	Val	Ser	Gln	Gly	Lys	Glu	Pro	Val
465							470					475			480
His	Leu	Leu	Ser	Leu	Phe	Lys	Asp	Lys	Pro	Leu	Ile	Ile	Tyr	Lys	Asn
				485					490					495	
Gly	Thr	Ser	Lys	Lys	Gly	Gly	Gln	Ala	Pro	Ala	Pro	Pro	Thr	Arg	Leu
			500						505					510	
Phe	Gln	Val	Arg	Arg	Asn	Leu	Ala	Ser	Ile	Thr	Arg	Ile	Val	Glu	Val
			515				520					525			
Asp	Val	Asp	Ala	Asn	Ser	Leu	Asn	Ser	Asn	Asp	Val	Cys	Val	Leu	Lys
			530				535					540			
Leu	Pro	Gln	Asn	Ser	Gly	Tyr	Ile	Trp	Val	Gly	Lys	Gly	Ala	Ser	Gln
545							550					555			560
Glu	Glu	Glu	Lys	Gly	Ala	Glu	Tyr	Val	Ala	Ser	Val	Leu	Lys	Cys	Lys
				565					570					575	
Thr	Leu	Arg	Ile	Gln	Glu	Gly	Glu	Glu	Pro	Glu	Glu	Phe	Trp	Asn	Ser
			580						585					590	

Leu Gly Gly Lys Lys Asp Tyr Gln Thr Ser Pro Leu Leu Glu Thr Gln
 595 600 605
 Ala Glu Asp His Pro Pro Arg Leu Tyr Gly Cys Ser Asn Lys Thr Gly
 610 615 620
 Arg Phe Val Ile Glu Glu Ile Pro Gly Glu Phe Thr Gln Asp Asp Leu
 625 630 635 640
 Ala Glu Asp Asp Val Met Leu Leu Asp Ala Trp Glu Gln Ile Phe Ile
 645 650 655
 Trp Ile Gly Lys Asp Ala Asn Glu Val Glu Lys Lys Glu Ser Leu Lys
 660 665 670
 Ser Ala Lys Met Tyr Leu Glu Thr Asp Pro Ser Gly Arg Asp Lys Arg
 675 680 685
 Thr Pro Ile Val Ile Ile Lys Gln Gly His Glu Pro Pro Thr Phe Thr
 690 695 700
 Gly Trp Phe Leu Gly Trp Asp Ser Ser Lys Trp
 705 710 715

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 16 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Leu Asn His Val Leu Thr Asn Asp Leu Thr Ala Lys Arg Leu Leu His
 1 5 10 15

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 16 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Lys Val Tyr Val Thr Glu Lys Val Ala Gln Ile Lys Gln Ile Pro Phe

1

5

10

15

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 782 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

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Met Ala Pro His Arg Pro Ala Pro Ala Leu Leu Cys Ala Leu Ser Leu
1      5      10      15
Ala Leu Cys Ala Leu Ser Leu Pro Val Arg Ala Ala Thr Ala Ser Arg
20      25      30
Gly Ala Ser Gln Ala Gly Ala Pro Gln Gly Arg Val Pro Glu Ala Arg
35      40      45
Pro Asn Ser Met Val Val Glu His Pro Glu Phe Leu Lys Ala Gly Lys
50      55      60
Glu Pro Gly Leu Gln Ile Trp Arg Val Glu Lys Phe Asp Leu Val Pro
65      70      75      80
Val Pro Thr Asn Leu Tyr Gly Asp Phe Phe Thr Gly Asp Ala Tyr Val
85      90      95
Ile Leu Lys Thr Val Gln Leu Arg Asn Gly Asn Leu Gln Tyr Asp Leu
100     105     110
His Tyr Trp Leu Gly Asn Glu Cys Ser Gln Asp Glu Ser Gly Ala Ala
115     120     125
Ala Ile Phe Thr Val Gln Leu Asp Asp Tyr Leu Asn Gly Arg Ala Val
130     135     140
Gln His Arg Glu Val Gln Gly Phe Glu Ser Ala Thr Phe Leu Gly Tyr
145     150     155     160
Phe Lys Ser Gly Leu Lys Tyr Lys Lys Gly Gly Val Ala Ser Gly Phe
165     170     175
Lys His Val Val Pro Asn Glu Val Val Val Gln Arg Leu Phe Gln Val
180     185     190
Lys Gly Arg Arg Val Val Arg Ala Thr Glu Val Pro Val Ser Trp Glu
195     200     205
Ser Phe Asn Asn Gly Asp Cys Phe Ile Leu Asp Leu Gly Asn Asn Ile
210     215     220
His Gln Trp Cys Gly Ser Asn Ser Asn Arg Tyr Glu Arg Leu Lys Ala
225     230     235     240

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Thr Gln Val Ser Lys Gly Ile Arg Asp Asn Glu Arg Ser Gly Arg Ala
 245 250 255
 Arg Val His Val Ser Glu Glu Gly Thr Glu Pro Glu Ala Met Leu Gln
 260 265 270
 Val Leu Gly Pro Lys Pro Ala Leu Pro Ala Gly Thr Glu Asp Thr Ala
 275 280 285
 Lys Glu Asp Ala Ala Asn Arg Lys Leu Ala Lys Leu Tyr Lys Val Ser
 290 295 300
 Asn Gly Ala Gly Thr Met Ser Val Ser Leu Val Ala Asp Glu Asn Pro
 305 310 315 320
 Phe Ala Gln Gly Ala Leu Lys Ser Glu Asp Cys Phe Ile Leu Asp His
 325 330 335
 Gly Lys Asp Gly Lys Ile Phe Val Trp Lys Gly Lys Gln Ala Asn Thr
 340 345 350
 Glu Glu Arg Lys Ala Ala Leu Lys Thr Ala Ser Asp Phe Ile Thr Lys
 355 360 365
 Met Asp Tyr Pro Lys Gln Thr Gln Val Ser Val Leu Pro Glu Gly Gly
 370 375 380
 Glu Thr Pro Leu Phe Lys Gln Phe Phe Lys Asn Trp Arg Asp Pro Asp
 385 390 395 400
 Gln Thr Asp Gly Leu Gly Leu Ser Tyr Leu Ser Ser His Ile Ala Asn
 405 410 415
 Val Glu Arg Val Pro Phe Asp Ala Ala Thr Leu His Thr Ser Thr Ala
 420 425 430
 Met Ala Ala Gln His Gly Met Asp Asp Asp Gly Thr Gly Gln Lys Gln
 435 440 445
 Ile Trp Arg Ile Glu Gly Ser Asn Lys Val Pro Val Asp Pro Ala Thr
 450 455 460
 Tyr Gly Gln Phe Tyr Gly Gly Asp Ser Tyr Ile Ile Leu Tyr Asn Tyr
 465 470 475 480
 Arg His Gly Gly Arg Gln Gly Gln Ile Ile Tyr Asn Trp Gln Gly Ala
 485 490 495
 Gln Ser Thr Gln Asp Glu Val Ala Ala Ser Ala Ile Leu Thr Ala Gln
 500 505 510
 Leu Asp Glu Glu Leu Gly Gly Thr Pro Val Gln Ser Arg Val Val Gln
 515 520 525
 Gly Lys Glu Pro Ala His Leu Met Ser Leu Phe Gly Gly Lys Pro Met
 530 535 540
 Ile Ile Tyr Lys Gly Gly Thr Ser Arg Glu Gly Gly Gln Thr Ala Pro
 545 550 555 560

Ala Ser Thr Arg Leu Phe Gln Val Arg Ala Asn Ser Ala Gly Ala Thr
 565 570 575
 Arg Ala Val Glu Val Leu Pro Lys Ala Gly Ala Leu Asn Ser Asn Asp
 580 585 590
 Ala Phe Val Leu Lys Thr Pro Ser Ala Ala Tyr Leu Trp Val Gly Thr
 595 600 605
 Gly Ala Ser Glu Ala Glu Lys Thr Gly Ala Gln Glu Leu Leu Arg Val
 610 615 620
 Leu Arg Ala Gln Pro Val Gln Val Ala Glu Gly Ser Glu Pro Asp Gly
 625 630 635 640
 Phe Trp Glu Ala Leu Gly Gly Lys Ala Ala Tyr Arg Thr Ser Pro Arg
 645 650 655
 Leu Lys Asp Lys Lys Met Asp Ala His Pro Pro Arg Leu Phe Ala Cys
 660 665 670
 Ser Asn Lys Ile Gly Arg Phe Val Ile Glu Glu Val Pro Gly Glu Leu
 675 680 685
 Met Gln Glu Asp Leu Ala Thr Asp Asp Val Met Leu Leu Asp Thr Trp
 690 695 700
 Asp Gln Val Phe Val Trp Val Gly Lys Asp Ser Gln Glu Glu Glu Lys
 705 710 715 720
 Thr Glu Ala Leu Thr Ser Ala Lys Arg Tyr Ile Glu Thr Asp Pro Ala
 725 730 735
 Asn Arg Asp Arg Arg Thr Pro Ile Thr Val Val Lys Gln Gly Phe Glu
 740 745 750
 Pro Pro Ser Phe Val Gly Trp Phe Leu Gly Trp Asp Asp Asp Tyr Trp
 755 760 765
 Ser Val Asp Pro Leu Asp Arg Ala Met Ala Glu Leu Ala Ala
 770 775 780

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 827 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Met Thr Lys Leu Ser Ala Gln Val Lys Gly Ser Leu Asn Ile Thr Thr
 1 5 10 15
 Pro Gly Leu Gln Ile Trp Arg Ile Glu Ala Met Gln Met Val Pro Val

20					25					30					
Pro	Ser	Ser	Thr	Phe	Gly	Ser	Phe	Phe	Asp	Gly	Asp	Cys	Tyr	Ile	Ile
		35					40					45			
Leu	Ala	Ile	His	Lys	Thr	Ala	Ser	Ser	Leu	Ser	Tyr	Asp	Ile	His	Tyr
	50					55					60				
Trp	Ile	Gly	Gln	Asp	Ser	Ser	Leu	Asp	Glu	Gln	Gly	Ala	Ala	Ala	Ile
65					70					75					80
Tyr	Thr	Thr	Gln	Met	Asp	Asp	Phe	Leu	Lys	Gly	Arg	Ala	Val	Gln	His
				85					90					95	
Arg	Glu	Val	Gln	Gly	Asn	Glu	Ser	Glu	Ala	Phe	Arg	Gly	Tyr	Phe	Lys
			100					105					110		
Gln	Gly	Leu	Val	Ile	Arg	Lys	Gly	Gly	Val	Ala	Ser	Gly	Met	Lys	His
		115					120					125			
Val	Glu	Thr	Asn	Ser	Tyr	Asp	Val	Gln	Arg	Leu	Leu	His	Val	Lys	Gly
	130					135					140				
Lys	Arg	Asn	Val	Val	Ala	Gly	Glu	Val	Glu	Met	Ser	Trp	Lys	Ser	Phe
145					150					155					160
Asn	Arg	Gly	Asp	Val	Phe	Leu	Leu	Asp	Leu	Gly	Lys	Leu	Ile	Ile	Gln
				165					170					175	
Trp	Asn	Gly	Pro	Glu	Ser	Thr	Arg	Met	Glu	Arg	Leu	Arg	Gly	Met	Thr
			180					185					190		
Leu	Ala	Lys	Glu	Ile	Arg	Asp	Gln	Glu	Arg	Gly	Gly	Arg	Thr	Tyr	Val
		195					200					205			
Gly	Val	Val	Asp	Gly	Glu	Asn	Glu	Leu	Ala	Ser	Pro	Lys	Leu	Met	Glu
	210					215					220				
Val	Met	Asn	His	Val	Leu	Gly	Lys	Arg	Arg	Glu	Leu	Lys	Ala	Ala	Val
225					230					235					240
Pro	Asp	Thr	Val	Val	Glu	Pro	Ala	Leu	Lys	Ala	Ala	Leu	Lys	Leu	Tyr
				245					250					255	
His	Val	Ser	Asp	Ser	Glu	Gly	Asn	Leu	Val	Val	Arg	Glu	Val	Ala	Thr
			260					265					270		
Arg	Pro	Leu	Thr	Gln	Asp	Leu	Leu	Ser	His	Glu	Asp	Cys	Tyr	Ile	Leu
		275					280					285			
Asp	Gln	Gly	Gly	Leu	Lys	Ile	Tyr	Val	Trp	Lys	Gly	Lys	Lys	Ala	Asn
	290					295					300				
Glu	Gln	Glu	Lys	Lys	Gly	Ala	Met	Ser	His	Ala	Leu	Asn	Phe	Ile	Lys
305					310					315					320
Ala	Lys	Gln	Tyr	Pro	Pro	Ser	Thr	Gln	Val	Glu	Val	Gln	Asn	Asp	Gly
				325					330					335	
Ala	Glu	Ser	Ala	Val	Phe	Gln	Gln	Leu	Phe	Gln	Lys	Trp	Thr	Ala	Ser
			340					345					350		

Asn Arg Thr Ser Gly Leu Gly Lys Thr His Thr Val Gly Ser Val Ala
 355 360 365
 Lys Val Glu Gln Val Lys Phe Asp Ala Thr Ser Met His Val Lys Pro
 370 375 380
 Gln Val Ala Ala Gln Gln Lys Met Val Asp Asp Gly Ser Gly Glu Val
 385 390 395 400
 Gln Val Trp Arg Ile Glu Asn Leu Glu Leu Val Pro Val Asp Ser Lys
 405 410 415
 Trp Leu Gly His Phe Tyr Gly Gly Asp Cys Tyr Leu Leu Leu Tyr Thr
 420 425 430
 Tyr Leu Ile Gly Glu Lys Gln His Tyr Leu Leu Tyr Val Trp Gln Gly
 435 440 445
 Ser Gln Ala Ser Gln Asp Glu Ile Thr Ala Ser Ala Tyr Gln Ala Val
 450 455 460
 Ile Leu Asp Gln Lys Tyr Asn Gly Glu Pro Val Gln Ile Arg Val Pro
 465 470 475 480
 Met Gly Lys Glu Pro Pro His Leu Met Ser Ile Phe Lys Gly Arg Met
 485 490 495
 Val Val Tyr Gln Gly Gly Thr Ser Arg Thr Asn Asn Leu Glu Thr Gly
 500 505 510
 Pro Ser Thr Arg Leu Phe Gln Val Gln Gly Thr Gly Ala Asn Asn Thr
 515 520 525
 Lys Ala Phe Glu Val Pro Ala Arg Ala Asn Phe Leu Asn Ser Asn Asp
 530 535 540
 Val Phe Val Leu Lys Thr Gln Ser Cys Cys Tyr Leu Trp Cys Gly Lys
 545 550 555 560
 Gly Cys Ser Gly Asp Glu Arg Glu Met Ala Lys Met Val Ala Asp Thr
 565 570 575
 Ile Ser Arg Thr Glu Lys Gln Val Val Val Glu Gly Gln Glu Pro Ala
 580 585 590
 Asn Phe Trp Met Ala Leu Gly Gly Lys Ala Pro Tyr Ala Asn Thr Lys
 595 600 605
 Arg Leu Gln Glu Glu Asn Leu Val Ile Thr Pro Arg Leu Phe Glu Cys
 610 615 620
 Ser Asn Lys Thr Gly Arg Phe Leu Ala Thr Glu Ile Pro Asp Phe Asn
 625 630 635 640
 Gln Asp Asp Leu Glu Glu Asp Asp Val Phe Leu Leu Asp Val Trp Asp
 645 650 655
 Gln Val Phe Phe Trp Ile Gly Lys His Ala Asn Glu Glu Glu Lys Lys
 660 665 670

Ala	Ala	Ala	Thr	Thr	Ala	Gln	Glu	Tyr	Leu	Lys	Thr	His	Pro	Ser	Gly	
		675					680					685				
Arg	Asp	Pro	Glu	Thr	Pro	Ile	Ile	Val	Val	Lys	Gln	Gly	His	Glu	Pro	
	690					695					700					
Pro	Thr	Phe	Thr	Gly	Trp	Phe	Leu	Ala	Trp	Asp	Pro	Phe	Lys	Trp	Ser	
705					710					715					720	
Asn	Thr	Lys	Ser	Tyr	Glu	Asp	Leu	Lys	Ala	Glu	Ser	Gly	Asn	Leu	Arg	
				725					730					735		
Asp	Trp	Ser	Gln	Ile	Thr	Ala	Glu	Val	Thr	Ser	Pro	Lys	Val	Asp	Val	
			740					745					750			
Phe	Asn	Ala	Asn	Ser	Asn	Leu	Ser	Ser	Gly	Pro	Leu	Pro	Ile	Phe	Pro	
		755					760					765				
Leu	Glu	Gln	Leu	Val	Asn	Lys	Pro	Val	Glu	Glu	Leu	Pro	Glu	Gly	Val	
	770					775						780				
Asp	Pro	Ser	Arg	Lys	Glu	Glu	His	Leu	Ser	Ile	Glu	Asp	Phe	Thr	Gln	
785					790					795					800	
Ala	Phe	Gly	Met	Thr	Pro	Ala	Ala	Phe	Ser	Ala	Leu	Pro	Arg	Trp	Lys	
				805					810					815		
Gln	Gln	Asn	Leu	Lys	Lys	Glu	Lys	Gly	Leu	Phe						
			820					825								

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 28 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "PRIMER"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

GATGCGGATC CAAYGAYYTN ACNGCNCA

28

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 28 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "PRIMER"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:
GATGCATCGA TACRTGNGCN ACYTTYTC

28

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "PRIMER"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:
CTCGAGGGTG GCGACGACTC C

21

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "PRIMER"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:
GCGGCCGCTT GACACCAGAC CAA

23

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "PRIMER"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

CAGCTATGAC CATGATTACG CCAA

24

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "PRIMER"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

ACGACGGCCA GTGAATTGCG TAAT

24

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Lys Val Ala Lys Val Glu Gln Val Lys Phe Asp Ala
1 5 10

Sequence Listing

	SEQ ID NO:	1
	Sequence length:	12
	Sequence Type:	amino acid
5	Topology:	linear
	Molecule type:	peptide
	Sequence description:	KVAHVKQIPFDA
	SEQ ID NO:	2
10	Sequence length:	9
	Sequence Type:	amino acid
	Topology:	linear
	Molecule type:	peptide
	Sequence description:	VLTNDLTAQ
15		
	SEQ ID NO:	3
	Sequence length:	5
	Sequence Type:	amino acid
	Topology:	linear
20	Molecule type:	peptide
	Sequence description:	ITNRK
	SEQ ID NO:	4
	Sequence length:	2418
25	Sequence Type:	nucleic acid
	Strandeness:	double
	Topology:	linear
	Molecule type:	cDNA

Sequence characteristic:

Symbol Showing Characteristic: mat peptide

Location: 27. . 2171

Sequence description:

CCGCCCGAAC ATCGCGTGCC CGAGTC ATG GCC CAG GGG CTG TAC CAC	47
Met Ala Gln Gly Leu Tyr His	
1 5	
GAG GAG TTC GCC CGC GCG GGC AAG CCG GCG GGG CTG CAG GTC TGG AGA	95
Glu Glu Phe Ala Arg Ala Gly Lys Arg Ala Gly Leu Gln Val Trp Arg	
10 15 20	
ATT GAG AAG CTG GAG CTG GTG CCG GTG CCC GAG AGC GCG TAT GGC AAC	143
Ile Glu Lys Leu Glu Leu Val Pro Val Pro Glu Ser Ala Tyr Gly Asn	
25 30 35	
TTC TAC GTC GGG GAT GCC TAC CTG GTG CTC CAC ACG ACG CAG GCC AGC	191
Phe Tyr Val Gly Asp Ala Tyr Leu Val Leu His Thr Thr Gln Ala Ser	
40 45 50 55	
CGG GGC TTC ACC TAC CGC CTG CAC TTC TGG CTG GGA AAG GAG TGT ACT	239
Arg Gly Phe Thr Tyr Arg Leu His Phe Trp Leu Gly Lys Glu Cys Thr	
60 65 70	
CAG GAT GAA AGC ACA GCA GCT GCC ATC TTT ACT GTT CAG ATG GAT GAC	287
Gln Asp Glu Ser Thr Ala Ala Ala Ile Phe Thr Val Gln Met Asp Asp	
75 80 85	
TAT TTG GGT GSC AAA CCT GTG CAG AAC AGA GAA CTT CAA GGC TAT GAG	335
Tyr Leu Gly Gly Lys Pro Val Gln Asn Arg Glu Leu Gln Gly Tyr Glu	
90 95 100	
TCT ACG GAT TTT GTT GGC TAC TTT AAA GGA GGT CTG AAA TAC AAG GCT	383
Ser Thr Asp Phe Val Gly Tyr Phe Lys Gly Gly Leu Lys Tyr Lys Ala	
105 110 115	
GGC GGT GTG GCG TCT GGA CTC AAT CAT GTG CTT ACA AAT GAC TTG ACT	431
Gly Gly Val Ala Ser Gly Leu Asn His Val Leu Thr Asn Asp Leu Thr	
120 125 130 135	
GCT CAG AGG CTC CTG CAT GTG AAA GGT CCG AGA GTC GTC AGG GCC ACG	479
Ala Gln Arg Leu Leu His Val Lys Gly Arg Arg Val Val Arg Ala Thr	
140 145 150	
GAA GTT CCC CTA AGC TGG GAC AGT TTC AAC AAG GGT GAC TGC TTC ATC	527
Glu Val Pro Leu Ser Trp Asp Ser Phe Asn Lys Gly Asp Cys Phe Ile	
155 160 165	
ATT GAC CTT GGC ACT GAA ATT TAC CAG TGG TGT GGA TCT TCT TGC AAC	575
Ile Asp Leu Gly Thr Glu Ile Tyr Gln Trp Cys Gly Ser Ser Cys Asn	
170 175 180	

AAG TAC GAG CGC CTG AAG GCC AGC CAG GTT GCC ATC GGC ATT CGG GAC Lys Tyr Glu Arg Leu Lys Ala Ser Gln Val Ala Ile Gly Ile Arg Asp 185 190 195	623
AAT GAA AGG AAA GGC AGA GCT CAG CTG ATT GTG GTA GAA GAA GGG AGT Asn Glu Arg Lys Gly Arg Ala Gln Leu Ile Val Val Glu Glu Gly Ser 200 205 210 215	671
GAA CCA TCA GAG CTT ACA AAG GTA TTA GGG GAA AAG CCA AAG CTT AGG Glu Pro Ser Glu Leu Thr Lys Val Leu Gly Glu Lys Pro Lys Leu Arg 220 225 230	719
GAT GGA GAA GAT GAT GAT GAC ATC AAA GCA GAT ATA ACT AAT AGG AAA Asp Gly Glu Asp Asp Asp Asp Ile Lys Ala Asp Ile Thr Asn Arg Lys 235 240 245	767
ATG GCT AAA CTC TAC ATG GTT TCA GAT GCC AGT GGC TCC ATG AAA GTG Met Ala Lys Leu Tyr Met Val Ser Asp Ala Ser Gly Ser Met Lys Val 250 255 260	815
AGT CTG GTG GCA GAA GAA AAC CCC TTC TCC ATG GCG ATG CTT CTG TCT Ser Leu Val Ala Glu Glu Asn Pro Phe Ser Met Ala Met Leu Leu Ser 265 270 275	863
GAA GAA TGC TTC ATT TTG GAC CAC GGT GCT GCA AAA CAG ATT TTT GTA Glu Glu Cys Phe Ile Leu Asp His Gly Ala Ala Lys Gln Ile Phe Val 280 285 290 295	911
TGG AAA GGT AAA GAT GCT AAT CCC CAG GAG AGA AAG GCT GCC ATG AAG Trp Lys Gly Lys Asp Ala Asn Pro Gln Glu Arg Lys Ala Ala Met Lys 300 305 310	959
ACA GCT GAG GAA TTC CTA CAG CAA ATG AAT TAT TCT ACG AAT ACC CAA Thr Ala Glu Glu Phe Leu Gln Gln Met Asn Tyr Ser Thr Asn Thr Gln 315 320 325	1007
ATT CAA GTT CTT CCA GAA GGA GGT GAA ACA CCA ATC TTC AAA CAG TTC Ile Gln Val Leu Pro Glu Gly Gly Glu Thr Pro Ile Phe Lys Gln Phe 330 335 340	1055
TTT AAG GAC TGG AGA GAT AGA GAT CAG AGC GAT GGC TTC GGG AAA GTG Phe Lys Asp Trp Arg Asp Arg Asp Gln Ser Asp Gly Phe Gly Lys Val 345 350 355	1103
TAT GTC ACA GAA AAA GTG GCT CAC GTA AAA CAA ATT CCA TTT GAT GCC Tyr Val Thr Glu Lys Val Ala His Val Lys Gln Ile Pro Phe Asp Ala 360 365 370 375	1151

TCA AAA TTG CAC AGC TCC CCA CAA ATG GCA GCC CAG CAT CAC GTG GTG	1199
Ser Lys Leu His Ser Ser Pro Gln Met Ala Ala Gln His His Val Val	
380 385 390	
GAT GAC GGT TCT GGC AAA GTG CAG ATT TGG CGT GTA GAA AAC AAC GGT	1247
Asp Asp Gly Ser Gly Lys Val Gln Ile Trp Arg Val Glu Asn Asn Gly	
395 400 405	
AGG GTC GAA ATT GAC CGA AAC TCG TAT GGT GAA TTC TAT GGT GGT GAT	1295
Arg Val Glu Ile Asp Arg Asn Ser Tyr Gly Glu Phe Tyr Gly Gly Asp	
410 415 420	
TGC TAC ATT ATA CTT TAC ACT TAT CCC AGA GGA CAG ATT ATC TAC ACC	1343
Cys Tyr Ile Ile Leu Tyr Thr Tyr Pro Arg Gly Gln Ile Ile Tyr Thr	
425 430 435	
TGG CAA GGA GCA AAT GCC ACA CGG GAT GAG CTG ACA ACC TCC GCA TTC	1391
Trp Gln Gly Ala Asn Ala Thr Arg Asp Glu Leu Thr Thr Ser Ala Phe	
440 445 450 455	
CTG ACT GTT CAG TTG GAT AGA TCC CTC GGG GGA CAG GCT GTG CAG ATT	1439
Leu Thr Val Gln Leu Asp Arg Ser Leu Gly Gly Gln Ala Val Gln Ile	
460 465 470	
CGA GTC TCC CAA GGC AAA GAA CCT GCT CAC CTG CTG AGT TTG TTC AAA	1487
Arg Val Ser Gln Gly Lys Glu Pro Ala His Leu Leu Ser Leu Phe Lys	
475 480 485	
GAC AAA CCG CTC ATT ATT TAC AAG AAC GGA ACA TCA AAG AAA GAA GGT	1535
Asp Lys Pro Leu Ile Ile Tyr Lys Asn Gly Thr Ser Lys Lys Glu Gly	
490 495 500	
CAG GCA CCA GCC CCC CCT ATA CGC CTC TTT CAA GTC CGA AGA AAC CTG	1583
Gln Ala Pro Ala Pro Pro Ile Arg Leu Phe Gln Val Arg Arg Asn Leu	
505 510 515	
GCT TCG ATC ACC AGA ATT ATG GAG GTA GAT GTT GAT GCA AAC TCA TTG	1631
Ala Ser Ile Thr Arg Ile Met Glu Val Asp Val Asp Ala Asn Ser Leu	
520 525 530 535	
AAT TCC AAT GAT GTT TTT GTC CTG AAA CTG CGA CAA AAT AAT GGC TAC	1679
Asn Ser Asn Asp Val Phe Val Leu Lys Leu Arg Gln Asn Asn Gly Tyr	
540 545 550	
ATC TGG ATA GGA AAA GGC TCC ACA CAG GAG GAG GAG AAA GGA GCA GAG	1727
Ile Trp Ile Gly Lys Gly Ser Thr Gln Glu Glu Glu Lys Gly Ala Glu	
555 560 565	

TAC GTG GCA AGC GTC CTC AAA TGC AAA ACT TCG ACG ATT CAG GAA GGC	1775
Tyr Val Ala Ser Val Leu Lys Cys Lys Thr Ser Thr Ile Gln Glu Gly	
570 575 580	
AAG GAA CCA GAG GAG TTT TGG AAT TCC CTT GGA GGG AAA AAA GAC TAC	1823
Lys Glu Pro Glu Glu Phe Trp Asn Ser Leu Gly Gly Lys Lys Asp Tyr	
585 590 595	
CAG ACC TCT CCT CTG CTA GAA TCC CAG GCT GAA GAC CAT CCA CCT CGG	1871
Gln Thr Ser Pro Leu Leu Glu Ser Gln Ala Glu Asp His Pro Pro Arg	
600 605 610 615	
CTT TAC GGC TGC TCC AAC AAA ACT GGA AGA TTC ATT ATT GAA GAG GTT	1919
Leu Tyr Gly Cys Ser Asn Lys Thr Gly Arg Phe Ile Ile Glu Glu Val	
620 625 630	
CCA GGA GAG TTC ACC CAG GAT GAT TTA GCA GAA GAT GAT GTC ATG CTG	1967
Pro Gly Glu Phe Thr Gln Asp Asp Leu Ala Glu Asp Asp Val Met Leu	
635 640 645	
TTA GAT GCT TGG GAA CAG ATT TTT ATT TGG ATT GGA AAA GAT GCC AAT	2015
Leu Asp Ala Trp Glu Gln Ile Phe Ile Trp Ile Gly Lys Asp Ala Asn	
650 655 660	
GAA GTT GAG AAA TCA GAA TCT CTG AAG TCT GCC AAA ATA TAC CTT GAG	2063
Glu Val Glu Lys Ser Glu Ser Leu Lys Ser Ala Lys Ile Tyr Leu Glu	
665 670 675	
ACC GAC CCT TCT GGA AGA GAC AAG AGG ACG CCA ATT GTC ATC ATA AAA	2111
Thr Asp Pro Ser Gly Arg Asp Lys Arg Thr Pro Ile Val Ile Ile Lys	
680 685 690 695	
CAG GGT CAT GAG CCA CCT ACT TTC ACA GGC TGG TTC CTG GGC TGG GAT	2159
Gln Gly His Glu Pro Pro Thr Phe Thr Gly Trp Phe Leu Gly Trp Asp	
700 705 710	
TCC AGC AGG TGG TAAACTGATT TTTGTAGGAA AAAACAAAT ATAATGGGGC	2211
Ser Ser Arg Trp	
715	
AGCTGTCCCA GGGGGGAAGG AGGAGCTTGT TTAACCTTAG AAAATTAACC TCAGCCATAT	2271
GGCTATTTTT CCGTGCTTAG AATTGGTTTG AAATTTCTTT TAAACTGGAA TTTTCTTATG	2331
TTAATATTTT TATAACTTTT CTATGGACC AATATTAGCT CTGCTGGATG CTGACATATC	2391
TTTATATATG ACTTTTFAAA GGGGCCG	2418

SEQ ID NO: 5
Sequence length: 2630
Sequence Type: nucleic acid
Strandeness: double
5 Topology: linear
Molecule type: cDNA
Sequence characteristic:
 Symbol Showing Characteristic: mat peptide
 Location: 79. . 2223
10 Sequence description:

AAGGTTCTCT CTGCTGCTCT CCGTTEAGTC CAAGATCAGC 40

GATATCAGCG GTCCCCCGGA GCATCGCGTG CAGGAGCC ATG GCG CCG GAG CTA TAC 96
Met Ala Arg Glu Leu Tyr
1 5

CAC GAA GAG TTC GCC CCG GCG GGC AAG CAG GCG GGG CTG CAG GTC TGG 144
His Glu Glu Phe Ala Arg Ala Gly Lys Gln Ala Gly Leu Gln Val Trp
10 15 20

AGG ATT GAG AAG CTG GAG CTG GTG CCC GTG CCC CAG AGC GCT CAC GGC 192
Arg Ile Glu Lys Leu Glu Leu Val Pro Val Pro Gln Ser Ala His Gly
25 30 35

GAC TTC TAC GTC GGG GAT GCC TAC CTG GTG CTG CAC ACG GCC AAG ACG 240
Asp Phe Tyr Val Gly Asp Ala Tyr Leu Val Leu His Thr Ala Lys Thr
40 45 50

AGC CGA GGC TTC ACC TAC CAC CTG CAC TTC TGG CTC GGA AAG GAG TGT 288
Ser Arg Gly Phe Thr Tyr His Leu His Phe Trp Leu Gly Lys Glu Cys
55 60 65 70

TCC CAG GAT GAA AGC ACA GCT GCT GCC ATC TTC ACT GTT CAG ATG GAT 336
Ser Gln Asp Glu Ser Thr Ala Ala Ala Ile Phe Thr Val Gln Met Asp
75 80 85

GAC TAT TTG GGT GGC AAG CCA GTG CAG AAT AGA GAA CTT CAA GGA TAT 384
Asp Tyr Leu Gly Gly Lys Pro Val Gln Asn Arg Glu Leu Gln Gly Tyr
90 95 100

GAG TCT AAT GAC TTT GTT AGC TAT TTC AAA GGC GGT CTG AAA TAC AAG 432
Glu Ser Asn Asp Phe Val Ser Tyr Phe Lys Gly Gly Leu Lys Tyr Lys
105 110 115

GCT GGA GGC GTG GCA TCT GGA TTA AAT CAT GTT CTT ACG AAC GAC CTG 480
Ala Gly Gly Val Ala Ser Gly Leu Asn His Val Leu Thr Asn Asp Leu
120 125 130

ACA GCC AAG AGG CTC CTA CAT GTG AAG GGT CGT AGA GTG GTG AGA GCC 528
Thr Ala Lys Arg Leu Leu His Val Lys Gly Arg Arg Val Val Arg Ala
135 140 145 150

ACA GAA GTT CCC CTT AGC TGG GAC AGT TTC AAC AAG GGT GAC TGC TTC 576
Thr Glu Val Pro Leu Ser Trp Asp Ser Phe Asn Lys Gly Asp Cys Phe
155 160 165

ATC ATT GAC CTT GGC ACC GAA ATT TAT CAG TGG TGT GGT TCC TCG TGC	624
Ile Ile Asp Leu Gly Thr Glu Ile Tyr Gln Trp Cys Gly Ser Ser Cys	
170 175 180	
AAC AAA TAT GAA CGT CTG AAG GCA AAC CAG GTA GCT ACT GGC ATT CGG	672
Asn Lys Tyr Glu Arg Leu Lys Ala Asn Gln Val Ala Thr Gly Ile Arg	
185 190 195	
TAC AAT GAA AGG AAA GGA AGG TCT GAA CTA ATT GTC GTG GAA GAA GGA	720
Tyr Asn Glu Arg Lys Gly Arg Ser Glu Leu Ile Val Val Glu Glu Gly	
200 205 210	
AGT GAA CCC TCA GAA CTT ATA AAG GTC TTA GGG GAA AAG CCA GAG CTT	768
Ser Glu Pro Ser Glu Leu Ile Lys Val Leu Gly Glu Lys Pro Glu Leu	
215 220 225 230	
CCA GAT GGA GGT GAT GAT GAT GAC ATT ATA GCA GAC ATA AGT AAC AGG	816
Pro Asp Gly Gly Asp Asp Asp Asp Ile Ile Ala Asp Ile Ser Asn Arg	
235 240 245	
AAA ATG GCT AAA CTA TAC ATG GTT TCA GAT GCA AGT GGC TCC ATG AGA	864
Lys Met Ala Lys Leu Tyr Met Val Ser Asp Ala Ser Gly Ser Met Arg	
250 255 260	
GTG ACT GTG GTG GCA GAA GAA AAC CCC TTC TCA ATG GCA ATG CTG CTG	912
Val Thr Val Val Ala Glu Glu Asn Pro Phe Ser Met Ala Met Leu Leu	
265 270 275	
TCT GAA GAA TGC TTT ATT TTG GAC CAC GGG GCT GCC AAA CAA ATT TTC	960
Ser Glu Glu Cys Phe Ile Leu Asp His Gly Ala Ala Lys Gln Ile Phe	
280 285 290	
GTA TGG AAA GGT AAA GAT GCT AAT CCC CAA GAG AGG AAG GCT GCA ATG	1008
Val Trp Lys Gly Lys Asp Ala Asn Pro Gln Glu Arg Lys Ala Ala Met	
295 300 305 310	
AAG ACA GCT GAA GAA TTT CTA CAG CAA ATG AAT TAT TCC AAG AAT ACC	1056
Lys Thr Ala Glu Glu Phe Leu Gln Gln Met Asn Tyr Ser Lys Asn Thr	
315 320 325	
CAA ATT CAA GTT CTT CCA GAA GGA GGT GAA ACA CCA ATC TTC AAA CAG	1104
Gln Ile Gln Val Leu Pro Glu Gly Gly Glu Thr Pro Ile Phe Lys Gln	
330 335 340	
TTT TTT AAG GAC TGG AGA GAT AAA GAT CAG AGT GAT GGC TTC GGG AAA	1152
Phe Phe Lys Asp Trp Arg Asp Lys Asp Gln Ser Asp Gly Phe Gly Lys	
345 350 355	

GTT TAT GTC ACA GAG AAA GTG GCT CAA ATA AAA CAA ATT CCC TTT GAT	1200
Val Tyr Val Thr Glu Lys Val Ala Gln Ile Lys Gln Ile Pro Phe Asp	
360 365 370	
GCC TCA AAA TTA CAC AGT TCT CCG CAG ATG GCA GCC CAG CAC AAT ATG	1248
Ala Ser Lys Leu His Ser Ser Pro Gln Met Ala Ala Gln His Asn Met	
375 380 385 390	
GTG GAT GAT GGT TCT GGC AAA GTG GAG ATT TGG CGT GTA GAA AAC AAT	1296
Val Asp Asp Gly Ser Gly Lys Val Glu Ile Trp Arg Val Glu Asn Asn	
395 400 405	
GGT AGG ATC CAA GTT GAC CAA AAC TCA TAT GGT GAA TTC TAT GGT GGT	1344
Gly Arg Ile Gln Val Asp Gln Asn Ser Tyr Gly Glu Phe Tyr Gly Gly	
410 415 420	
GAC TGC TAC ATC ATA CTC TAC ACC TAT CCC AGA GGA CAG ATT ATC TAC	1392
Asp Cys Tyr Ile Ile Leu Tyr Thr Tyr Pro Arg Gly Gln Ile Ile Tyr	
425 430 435	
ACG TGG CAA GGA GCA AAT GCC ACA CGA GAT GAG CTG ACA ACA TCT GCG	1440
Thr Trp Gln Gly Ala Asn Ala Thr Arg Asp Glu Leu Thr Thr Ser Ala	
440 445 450	
TTC CTG ACT GTT CAG TTG GAT CGG TCC CTT GGA GGA CAG GCT GTG CAG	1488
Phe Leu Thr Val Gln Leu Asp Arg Ser Leu Gly Gly Gln Ala Val Gln	
455 460 465 470	
ATC CGA GTC TCC CAA GGC AAA GAG CCT GGT CAC CTA CTG AGT TTG TTC	1536
Ile Arg Val Ser Gln Gly Lys Glu Pro Val His Leu Leu Ser Leu Phe	
475 480 485	
AAA GAC AAA CCG CTC ATT ATT TAC AAG AAT GGA ACA TCA AAG AAA GCA	1584
Lys Asp Lys Pro Leu Ile Ile Tyr Lys Asn Gly Thr Ser Lys Lys Gly	
490 495 500	
GGT CAG GCA CCT GCT CCC CCT ACA CGC CTC TTT CAA GTC CGG AGA AAC	1632
Gly Gln Ala Pro Ala Pro Pro Thr Arg Leu Phe Gln Val Arg Arg Asn	
505 510 515	
CTG GCA TCT ATC ACC AGA ATT GTG GAG GTT GAT GTT GAT GCA AAT TCA	1680
Leu Ala Ser Ile Thr Arg Ile Val Glu Val Asp Val Asp Ala Asn Ser	
520 525 530	
CTG AAT TCT AAC GAT GTT TGT GTC CTG AAA CTG CCA CAA AAT AGT GGC	1728
Leu Asn Ser Asn Asp Val Cys Val Leu Lys Leu Pro Gln Asn Ser Gly	
535 540 545 550	

TAC ATC TGG GTA GGA AAA GGT GCT AGC CAG GAG GAG GAG AAA GGA GCA	1776
Tyr Ile Trp Val Gly Lys Gly Ala Ser Gln Glu Glu Glu Lys Gly Ala	
555 560 565	
GAG TAT GTA GCA AGT GTC CTA AAG TGC AAA ACC TTA AGG ATC CAA GAA	1824
Glu Tyr Val Ala Ser Val Leu Lys Cys Lys Thr Leu Arg Ile Gln Glu	
570 575 580	
GGC GAG GAG CCA GAG GAG TTC TGG AAT TCC CTT GGA GGG AAA AAA GAC	1872
Gly Glu Glu Pro Glu Glu Phe Trp Asn Ser Leu Gly Gly Lys Lys Asp	
585 590 595	
TAC CAG ACC TCA CCA CTA CTG GAA ACC CAG GCT GAA GAC CAT CCA CCT	1920
Tyr Gln Thr Ser Pro Leu Leu Glu Thr Gln Ala Glu Asp His Pro Pro	
600 605 610	
CGG CTT TAC GGC TGC TCT AAC AAA ACT GGA AGA TTT GTT ATT GAA GAG	1968
Arg Leu Tyr Gly Cys Ser Asn Lys Thr Gly Arg Phe Val Ile Glu Glu	
615 620 625 630	
ATT CCA GGA GAG TTC ACC CAG GAT GAT TTA GCT GAA GAT GAT GTC ATG	2016
Ile Pro Gly Glu Phe Thr Gln Asp Asp Leu Ala Glu Asp Asp Val Met	
635 640 645	
TTA CTA GAT GCT TGG GAA CAG ATA TTT ATT TGG ATT GGC AAA GAT GCT	2064
Leu Leu Asp Ala Trp Glu Gln Ile Phe Ile Trp Ile Gly Lys Asp Ala	
650 655 660	
AAT GAA GTT GAG AAA AAA GAA TCT CTG AAG TCT GCC AAA ATG TAC CTT	2112
Asn Glu Val Glu Lys Lys Glu Ser Leu Lys Ser Ala Lys Met Tyr Leu	
665 670 675	
GAG ACA GAC CCT TCT GGA AGA GAC AAG AGG ACA CCA ATT GTC ATC ATA	2160
Glu Thr Asp Pro Ser Gly Arg Asp Lys Arg Thr Pro Ile Val Ile Ile	
680 685 690	
AAA CAG GGC CAT GAG CCA CCC ACA TTC ACA GGC TGG TTC CTG GCC TGG	2208
Lys Gln Gly His Glu Pro Pro Thr Phe Thr Gly Trp Phe Leu Gly Trp	
695 700 705 710	
GAT TCC AGC AAG TGG TAAATTGGTA TTTGTAAAAA GCAAACAAAC ATTACAAGGC	2263
Asp Ser Ser Lys Trp	
715	
AGTTATCTCA TTGCTGTTTT GCGAGAGGAA CGGGAAAAGC TTTTGTCTTA TTGTCTTTTT	2323
GAAAATTAAAG GCTGGGCGCG GTGGCTCACA CCTGTAAATCC CAGCACTTTG AGAGGATGAG	2383

GTAGGCGGAT CACTGGGGTC AGGATTTCGA GACCAGCCTG GCCAACATGG CGAAACCTCG 2443
 CCTCTACTAA AAATACAAAA AAATTAGCTG CGCGTGGTGG TGCACGCCTG TAGTCCCTGC 2503
 TACTTGGGAG GCTGAGACAG GAAAATTGCT TGAGCCGAGG AGGCTGAGGT TGCAGTGAGC 2563
 CAGGATTGGG CCACCACACT CCAGCCTGGG CAACAGAGAC TCTGTCTCAA AAAAAAAAAA 2623
 AAAAAAA 2630

	SEQ ID NO:	6
	Sequence length:	16
	Sequence Type:	amino acid
	Topology:	linear
5	Molecule type:	peptide
	Sequence description:	LNHVLTNDLTAKRLLH
	SEQ ID NO:	7
	Sequence length:	16
10	Sequence Type:	amino acid
	Topology:	linear
	Molecule type:	peptide
	Sequence description:	KVYVTEKVAQIKQIPF